## AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application.

**Listing Of Claims**

1. (original) A composition comprising a protein in crystalline form wherein the protein has at least 90% identity with residues 143-438 of SEQ. ID No. 1.

2. (original) A composition according to claim 1 wherein the protein has at least 95% identity with residues 143-438 of SEQ. ID No. 1.

3. (original) A composition according to claim 1 wherein at least a portion of the protein comprises consecutively residues 143-438 of SEQ. ID No. 1.

4. (original) A composition according to claim 1 wherein the protein crystal diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

5. (original) A composition according to claim 1 wherein the protein crystal has a crystal lattice in a $P2_12_12_1$ space group.

6. (original) A composition according to claim 1 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=48.36Å b=72.29Å and c=94.52Å, $\alpha=\beta=\gamma=90^\circ$.

7. (original) A composition comprising AKT3 in crystalline form wherein the crystal has a crystal lattice in a $P2_12_12_1$ space group.

8. (original) A composition comprising AKT3 in crystalline form wherein the crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=48.36Å b=72.29Å and c=94.52Å, $\alpha=\beta=\gamma=90^\circ$.

9. (original) A method for forming a crystal of a protein comprising:

forming a crystallization volume comprising: a precipitant solution and a protein wherein the protein has at least 90% identity with residues 143-438 of SEQ. ID No. 1; and

storing the crystallization volume under conditions suitable for crystal formation of the protein.

10. (original) A method according to claim 9 wherein the protein has at least 95% identity with residues 143-438 of SEQ. ID No. 1.

11. (original) A method according to claim 9 wherein at least a portion of the protein comprises consecutively residues 143-438 of SEQ. ID No. 1.

12. (original) A method according to claim 9 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

13. (original) A method according to claim 9 wherein the protein crystal has a crystal lattice in a $P2_12_12_1$ space group.

14. (original) A method according to claim 9 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=48.36Å b=72.29Å and c=94.52Å, $\alpha=\beta=\gamma=90^{\circ}$.

15. (original) A method according to claim 9, the method further comprising diffracting the protein crystal to produce a diffraction pattern and solving the structure of the protein from the diffraction pattern.

16. (original) A composition comprising at least a portion of a protein expressed as a nucleic acid molecule that comprises SEQ. ID No. 2.

17. (withdrawn) A composition comprising an isolated protein consisting of SEQ. ID No. 3.

18. (withdrawn) A method of identifying an entity that associates with a protein comprising:

taking structure coordinates from diffraction data obtained from a crystal of a protein that has at least 90% identity with SEQ. ID No. 3; and

performing rational drug design using a three dimensional structure that is based on the obtained structure coordinates.

19. (withdrawn) A method according to claim 18 wherein the protein has at least 95% identity with SEQ. ID No. 3.

20. (withdrawn) A method according to claim 18 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=48.36Å b=72.29Å and c=94.52Å, $\alpha=\beta=\gamma=90^{o}$.

21. (withdrawn) A method according to claim 18 wherein the protein crystal has a crystal lattice in a $P2_12_12_1$ space group

22. (withdrawn) A method according to claim 18, the method further comprising selecting one or more entities based on the rational drug design and contacting the selected entities with the protein.

23. (withdrawn) A method according to claim 18, the method further comprising measuring an activity of the protein when contacted with the one or more entities.

24. (withdrawn) A method according to claim 18, the method further comprising comparing activity of the protein in a presence of and in the absence of the one or more entities; and selecting entities where activity of the protein changes depending whether a particular entity is present.

25. (withdrawn) A method according to claim 18, the method further comprising contacting cells expressing the protein with the one or more entities and detecting a change in a phenotype of the cells when a particular entity is present.